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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 100243

TO: Vanessa L Ford

Location: cm-1/8A16/8E12

Art Unit: 1645

Aug 4____, 2003

Case Serial Number: 10/017168

From: P. Sheppard Location: CM1-1E03 Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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From: Sent:

Subject:

Chan, Christina

To:

Thursday, July 31, 2003 3:35 PM Ford, Vanessa; STIC-Biotech/ChemLib RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Ford, Vanessa

Sent:

Thursday, July 31, 2003 2:49 PM

To:

Chan, Christina

Subject:

In re: 10/017168 sequence search

Please search SEQ ID NO:15. Please include interference searches. Please rush!

Vanessa L. Ford

Biotechnology Patent Examiner

Office: CM1 8A16 Mailbox: CM1 8E12 Phone: 703.308.4735



Searcher:	
Phone:	
Location:	
Date Picked Up:_	
Date Completed:	8/4/03
Searcher Prep/Re	view:
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

'ENDOR/COST (where applic.)
STN:
DIALOG:
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DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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"Acidic repeat protein (arp) gene sequence of Treponema pallidum subspecies pertenue (CDC 2 strain).";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR342806; AAK01460.2; -.

SEQUENCE 348 AA; 37936 MW; E4A446BD82344592 CRC64;
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"Molecular characterization o
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EMBL; AF411126; AAL07373.1; -.
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                             O83448 PRELIMINARY;
O83448;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treponema pallidum.";

Treponema pallidum.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF411124; AAL07372.1; -.

SEQUENCE 548 AA; 59405 MW; 1F6B5BBB04D41D13 CRC64;
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Q93CA4;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-QCT-2002 (TrEMBLrel. 22,
SEQUENCE FROM N.A.
STRAIN-Nichols;
MEDIANE=98323770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinsto
                                                                                                                                          Treponema pallidum.
Bacteria; Spirochaetes;
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum subsp. pallidum (syphilis treponeme).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae;
NCBI_TaxID=161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARP.
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01-OCT-2002 (TrEMBLrel.
Acidic repeat protein.
                                                                                                                                                                                                                                      Hypothetical TP0433.
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Bacteria; Spirochaetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF015824; AAB94541.1; SEQUENCE 432 AA; 46364 M
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llarity 100.0%;
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Pred. No. 2.8e-07
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Pred. No. 3.6e-07;
; Mismatches 0;
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RESULT
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Q9SIJ8;
01-MAY-2000
01-JUN-2002
01-OCT-2002
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01-MAR-2002
                               Expressed
AT2G21620.
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EMBL; AE001220; AAC65421.1; -.
TIGR; TP0433; -.
Hypothetical protein; Complete
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MEDLINE=98332770; PubMed=9665876;
   Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 2
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EMBL; AE001220; AAC65422.1;
TIGR; TP0434; -
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Bacteria; Spirochaetès;
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256 AA; 27453 MW;
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227 AA; 25035 MW; 3FA02711A86E45FE
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01-DEC-2001
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Barnstead M.E., Mason T.M., Bowman C.L
Carrera A.J., Creasy T.H., Buell C.R.,
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMEMBL; AC007119; AAD23643.2; -. EMBL; AY087097; AAM64657.1; -.
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                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Feldmann K.A., Flavell R.B.
"Full-length messenger RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv.
                                  Plant Cell Physiol. 33:217-224(1992)
EMBL; AB039925; BAB63912.1; -.
                                                        protein.";
                                                                   of one cDNA clone that
                                                                             "Molecular cloning and charac
responsive to desiccation in
                                                                                                                                                    Submitted
                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Columbia;
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Brover V., Troukhan M.,
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                     InterPro;
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                     IPR006016;
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(TrEMBLrel. 22,
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 21253 MW;
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                                                                             , Koizumi M., Urao S., Shinozaki K.;
characterization of 9 cDNAs for genes that are
ion in Arabidopsis thaliana: sequence analysis
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White O., Salzberg S.L.;
equences greatly improve genome
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A Strausberg R.;

L Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC018938; AAH18938.1; -.

R InterPro; IPR000345; CytC heme bind.

R InterPro; IPR002219; DAG PE-bind.

R InterPro; IPR001841; Znf ring.

R InterPro; IPR001841; Znf ring.

R ROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00181; DAG PE BIND DOM 2; 1.

DR PROSITE; PS00089; Zr RING 2; 1.

DR PROSITE; PS00089; Zr RING 2; 1.

SC SEQUENCE 256 AA; Z9724 MW; 3433001005D7EDDF CRC64;
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Matches 10
                            MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TERMBLrel. 03, Created)
01-MAY-1997 (TERMBLrel. 23, Last sequence update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Hypothetical 58.3 kDa protein (Phosphoglucomutase).
PGMA OR RV3068C OR MTCY22D7.13 OR MT3153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TREMBLrel. 23, Last annotation update)
Similar to RIKEN cDNA 2510027N19 gene.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WV22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriae; Mycobacteriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Pred. No.
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RESULT 13
Q8CPY0
ID Q8CPY
AC Q8CPY
DT 01-M2
DT 01-M2

Q8CPY0; Q8CPY0; 01-MAR-2003 01-MAR-2003

(TrEMBLrel. (TrEMBLrel.

23,

Created) Last seq

sequence update)

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RESULT 12
Q8IBW7
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Best Local S
Matches 9
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Best Local Similarity
Matches 10; Conserv
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Q8IBW7;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                   Seeger K., Murphy L., Harri
Quail M., Barrell B.;
Submitted (SEP-2002) to the
                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; H
MCBI_TaxID=36329;
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Pfam; PF02878; PGM PMM I; 1.
Pfam; PF02879; PGM PMM II; 1.
Pfam; PF02880; PGM PMM III; 1.
PTGREPAMS; TIGR01132; PGM; 1.
PROSITE; PS00710; PGM PMM; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Tomplete proteome.
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A.,
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Erythrocyte MAL7P1.56.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; MT3153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
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                                                                                                                                                                                         AL844506; CAD50877.1;
NCE 2192 AA; 248940
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                                                                                           Similarity
9; Conserv
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p; IPR005852; Pglucomut A.
p; IPR005844; PG PMM ABAII.
p; IPR005844; PG PMM ABAII.
p; IPR005846; PG PMM ABAIII.
p; IPR005846; PG PMM ABAIII.
                      EVEDVPKVVEPASERE 16
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EEKEAPKVVEPAVKKE
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                                                                                             Conservative
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                                                                                                            47.5%;
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  892
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                                                                                           Score 48; DB
Pred. No. 2.5e
4; Mismatches
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Last annotation update)
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Pred. No. 56;
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RESULT 14
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Earsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Earsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashina J., Mazarelli J., Mombaerte P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashi T., Kill Y., Kohtsuki S.,
  Query Match
Best Local S
Matches 8
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                         InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR002219; DAG_PE_bind.
PROSITE; PS00190; CYTCCHROME C; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
SEQUENCE 266 AA; 30708 MW; F5728C530532E03A CRC64;
                                                                                                                                                                                    EMBL; AK009715; br
MGD; MGI:1914961;
                                                                                                                                                                                                                          Hayashizaki Y.; "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Zhang Y., Ren S., Li H.,
Chen Z., Wen Y.;
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Bacteria; Firmicutes; Bacil
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031848; AAH31848.1; -.
InterPro; IPR00345; CytC heme bind.
InterPro; IPR002219; DAG PE-bind.
PROSITE; PS00190; CYTOCHROME C; 1.
PROSITE; PS00081; DAG PE BIND DOM 2; 1.
SEQUENCE 280 AA; 37038 MW; CC5BCCC949EA269F CRC64;
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RF2 CORGL
ME31 DROME
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DR PIR; C35147; C35147.

DR InterPro; IPR002104; Phage integrase: 1.

Pfam; PP00589; Phage integrase: 1.

TRANSIENT COVALENT LINKAGE TO DNA STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).

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P49754; Q99851; Q99852;
01-CCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vacuelar assembly protein VPS41 homolog (S53).
VPS41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of the genetic elements required for site-specific integration of plasmid pSE211 in Saccharopolyspora erythraea.";

J. Bacteriol. 172:1877-1888(1990).
-I- FUNCTION: Is a recombinase (or integrase), catalyzing the cutting and rejoining of the recombining DNA molecules.
-I- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
Sherrington
                                                                                                    Radisky D.C., Snyder W.B., Emr S.D., Kaplan J.; "Characterization of VPS41, a gene required for vacuolar trafficking and high-affinity iron transport in yeast."; Proc. Natl. Acad. Sci. U.S.A. 94:5662-5666(1997).
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
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MEDLINE=90202705; PubMed=2180909;

Brown D.P., Idler K.B., Katz L.;
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                      MEDLINE=95319502; PubMed=7596406;
                                                                                                                                                                                             MEDLINE=97303186; PubMed=9159129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharopolyspora erythraea (Streptomyces erythraeus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrase
                                              FISSUE=Brain;
                                                                                                                                                                                                                     IISSUE=Heart;
                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1836;
                                                                  EQUENCE OF 615-744 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVEDVPKVVEPASEREGGER 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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EVEDMQLVIKAALERRNGVR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Recombinase).
  R., Rogaev E.I., Liang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 19, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                     Chordata;
Primates;

 Mismatches

                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
Rogaeva E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
  Levesque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cutting
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RESULT 4 VG72_HSVI

2_HSVI1 VG72_HSVI1 Q00103; 01-DEC-1992

STANDARD;

1350

01-DEC-1992 01-DEC-1992

(Rel. (Rel. (Rel.

24, Created)24, Last sequence update)24, Last annotation updat72 protein.

update)

Hypothetical

gene

Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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                                                   S
                                                                                                                                                                                                                        Matches
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMO0299; CLH; 1.
SMART; SM00299; CLH; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING_1; FALSE NEG.
PROSITE; PS50089; ZE RING_2; 1.
Zinc-finger; Alternative splicing.
791 839 RING-TYPE.
                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000547; Clathrin_repeat.
InterPro; IPR001841; Znf_ring.
Pfam; PF00637; Clathrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U87309; AAB47563.1; -.
EMBL; U87281; AAB47758.1; -.
EMBL; L40398; AAC42004.1; -.
Genew; HGNC:12713; VPS41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 375:754-760(1995).
-!- FUNCTION: REQUIRED FOR VACUOLAR ASSEMBLY AND VACUOLAR TRAFFIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Polinsky R.J., Wasco W., da Silva H.A.R., Hair Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 605485; -.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0005478; F:intracellular transporter activity; TAS.

GO; GO:0007034; P:vacuolar transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease."
                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a gene bearing missense mutations in early-onset familial
                                                                                                                                                                                                                                                                                                                                                                                                                 MAIN
                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P49754-2; Sequence=VSP_006751, VSP_006752; SIMILARITY: BELONGS TO THE VPS41 FAMILY. SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative
676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P49754-1; Sequence=Displayed
                                                                                                         Similarity 9; Conserv
                                                      EVEDVPKVVEPASEREGGE
ELHDVDKAIEFAKEQDDGE
                                                                                                                                                                                                                  615
736
854 AA;
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                 803
                                                                                                                                                                                                                                                  618
744
                                                                                                                                                                                                                                                                                                                               854
                                                                                                                                                                                                                                                                                                                                                                                     802
                                                                                                                                     45.5%;
                                                                                                                                                                                                                        98535 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing; Named isoforms=2;
                                                                                                                                                                                                                  /FTId=VSP 006751.

Missing (In isoform Short).
/FTId=VSP 006752.

KQIS -> wHEG (IN REF. 2).
IPNLRDSLV -> DPOFERFLG (IN RIPNLRDSLV -> DFOFERFLG (IN RIPNLRDSLV -> DFOFERFL 
                                                                                                         4.
                                                                                                                                   Score 46;
Pred. No.
                                                      19
  694
                                                                                                                                                                                                                                                                                                                                                                               POLY-GLU.
D -> E (in isoform
                                                                                                            Mismatches
                                                                                                                                        31;
                                                                                                                                                                  BB
                                                                                                                                                                  μ,
                                                                                                            6,
                                                                                                                                                                  Length 854;
                                                                                                                                                                                                                                                                                                                                                                                     Short).
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haines J.L.,
                                                                                                                                                                                                                                               REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.F.
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                                                                                                            Gaps
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel.
01-NOV-1990 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no cestrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         EMBL; M36177; AAA72862.1; PIR; C36044; C36044.
                                                                                                or send an
                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                            the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                         volcanii.";
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                          MEDLINE=90370836; PubMed=2118654;
                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                   Halobacterium volcanii (Haloferax volcanii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRPC_HALVO
P18304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007087; Znf_C2H2.
SMART; SM00355; Znf_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M75136; AAA88174.1; -. PIR; G36793; G36793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
STRAIN=Auburn
HSSP; Q06121; 1A53.
HAMAP; MF 00134; -; 1.
InterPro; IPR003009; FMN enzyme.
InterPro; IPR001468; IGPS.
                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 186:9-14(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davison A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                    "Genes for tryptophan
                                                                                                                                                                                                                                                                                                                   Lam W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indole-3-glycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Channel catfish virus: a new type of herpesvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ictalurid
                                                                                                                                                                                                               PATHWAY: Tryptophan biosynthesis; fourt SIMILARITY: BELONGS TO THE TRPC FAMILY.
                                                                                                                                                                                                                                          c. Natl. Acad. Sci. U.S.A. 87:6614-6618(1990).
CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose
phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO[(2) + H(2)0.
                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSVKRRIEAASKMEGGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDVPKVVEPASEREGGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                 Cohen A., Tsouluhas D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes-like viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein.
1350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             16, Last sequence v
41, Last annotation
phosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                    biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ED4780D2F2900FFD CRC64;
                                                                                                                                                                                                                                                                                                                Doolittle
                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 4.1.1.48) (IGPS).
                                                                                                                                                                                                                             fourth step.
                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                        Halobacteriales;
                                                                                                               noved. Usage by and for commercial (See http://www.imb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                    archaebacterium
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                                                                                                                                                                                                                                                                                                    Haloferax
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                                                                                                                                                                      collaboration -
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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ProDom; PD001511; IGPS; 1.
PROSITE; PS00614; IGPS; 1.
Tryptophan biosynthesis; Lyase; Decarboxylase.
SEQUENCE 251 AA; 26754 MW; 2F2FD9E702B4800
                                                                                                                                                                                                                                                                        modulator (CREM) gene ";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
-SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA,
BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
-!- SUBUNIT: Binds DNA as a dimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93096608; PubMed=1461747;
Meyer T.E., Habener J.F.;
"Cyclic AMP response element binding protein CREB and modulator
protein CREM are products of distinct genes.";
Nucleic Acids Res. 20:6106-6106(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
CAMP responsive element modulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human CREM gene: evolutionary conservation, chromosomal localization, and inducibility of the transcript."; Cell Growth Differ. 4:931-937(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREM HUMAN STANDARD; P. 003060; Q16114; Q16116; Q9NZB9; 01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-232 FROM Vouk K., Lalli B., Sche Komel R., Rozman D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94128610; PubMed=7916662; Masquilier D., Foulkes N.S., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREM HUMAN
                                                                                                                                                                                                                                                                                                                                                                                      "Searching for mutations in the human cAMP responsive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Na
                                                                        PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                    Name=Gamma;
                                                                                                       IsoId=Q03060-3;
                                                                                                                                                                                               IsoId=Q03060-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                    IsoId=Q03060-4;
                                                                                                                                                                 IsoId=Q03060-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVPKVVEPASEREGGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVRAILEAARÉRPGGE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Scherer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.6%;
                                                                                                       Sequence=Not described;
                                                                                                                                    Sequence=Not described;
                                                                                                                                                               Sequence=VSP_000599, VSP_000600, VSP_000601;
                                                                                                                                                                                              Sequence=Displayed;
                                                                                                                                                                                                                            splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   S.W., Sassone-Corsi P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2F2FD9E702B48065 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 AA
                                                                                       (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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                                                                                                                                                                                                                      RESULT 7
CREM_CANFA
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z15159; CAA78858.1; -.
EMBL; S68134; AAC60617.2; -.
EMBL; S68271; AAC60616.2; ALT SEQ.
EMBL; AF213899; AAF68266.2; JOINED.
EMBL; AF213899; AAF68266.2; JOINED.
EMBL; AF213898; AAF68266.2; JOINED.
P79145;
15-JUL-1998.
15-JUL-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
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CONFLICT
SEQUENCE
                                                                                                                                                                                                            CREM_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00170; bZIP; 2.—
Pfam; PF02173; pKID; 2.
PRINTS; PR00041; LUZZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                 TISSUE=Thyroid;
MEDLINE=97410117; PubMed=9266832;
                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                    CREM.
                                                                                                                                                           cAMP responsive element modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Repressor; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:2352; CREM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                        SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=9615;
                                                                                                                                        Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; TAS.
GO; GO:0007165; P:signal transduction;
InterPro; IPR001330; Leuzip_CREB.
InterPro; IPR003102; pKID.
InterPro; IPR004827; TF bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123812;
                                                                                                                                                                                                                                                              131
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Alternative splicing.
275 296 BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              DVPGVPKIEEERSEEEG 147
                                                                                                                                                                                                                                                                                 EVEDVPKVVEPASEREG 17
                                                                                                                                                                                                                                                                                                                                           41
332
332 AA;
                                                                                                                                                                    (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                     333
345
332
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90
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                                                                                                                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                            35531 MW;
                                                                                                                                                                                                                                                                                                               52.9%;
                                                                                                                                                                                                                                                                                                                        43.6%;
                                                                                                                                                                                                                                                                                                                                                     /FIId=VSP_000600.
A -> T (in isoform Alpha).
/FIId=VSP_000601.
N -> I (IN REF. 2).
A -> R (IN REF. 1).
VSVAG -> CSELR (IN REF. 2).
D -> DY (IN REF. 2).
                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                               Score 44; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                        Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUCINE-ZIPPER (BY SIMILARITY).
Missing (in isoform Alpha).
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP
                                                                                                                                                                                                                                                                                                                                            1D014C2EA416D72A CRC64;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                             344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       (In isoform Alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                    000599
                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                       Length 332
                                                 distribution,
        (CRE), A
CREM ALPHA
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RESULT 8
AMPH_CHICK
ID AMPH_CHICK
AC P50478;
DT 01-CCT-1996
DT 01-CCT-1996
DT 01-SEP-2003
DE Amphi.Dhysin.
GN AMPH.
OS Gallus gallı
CS Gallus gallı
CC Archosauria.
OC Archosauria.
OC Archosauria.
OC Archosauria.
CC STRALN=Tetri
RX MEDLINE=923:
RA Lichte B., 1
RI EMBO J. 11:
CHICKETO
                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                               Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Nachomenria: Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                               01-OCT-1996
01-OCT-1996
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a copyre the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
              Lichte B., Veh R.W., Meyer H.E., Kilimann M.W.; "Amphiphysin, a novel protein associated with synaptic vesicles."; EMBO J. 11:2521-2530(1992).
                                                      SEQUENCE FROM N.A.
STRAIN=Tetra-hybrid;
MEDLINE=92331604; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00170; bZIP; 1.
Pfam; PF02173; pKID; 1.
PRINTS; PR00041; LEUZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X99115; CAA67563.1; -. PIR; JC5601; JC5601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    +++
                                                                                                                                                                                                  Amphiphysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001630; Leuzip_CREB.
InterPro; IPR003102; pKID.
InterPro; IPR004827; TF_bZIP.
                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PTM: STIMULATED BY PHOSPHORYLATION (BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Binds DNA as a dimer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
    FUNCTION: MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTIONAL RESPONSE,
                                                                                                                                                                                                                                                                                                                                          131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P79145-4; Sequence=Not described;
M: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P79145-3;
                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P79145-1;
                                                                                                                                                                                                                                                                                                                                            DVPGVPKIEEEKSEEEG
                                                                                                                                                                                                                                                                                                                                                                     EVEDVPKVVEPASEREG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
                                                                                                                                                                                                                 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                              34, Created)
34, Last sequence 42, Last annotations
    PARTICIPATE IN MECHANISMS OF REGULATED EXOCYTOSIS IN
                                                       PubMed=1628617;
                                                                                                                                                                                                                                                                                                                                                                                                               43.6%;
52.9%;
                                                                       TISSUE=Forebrain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TF_bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=Not
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                                                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                               sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHILE
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                       682
                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 344;
                                                                                                                                            Phasianinae;
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SYV METTH 1D SYV METH 1D SYV METH 1D SYV AC 0268 OF 16-C DT 16
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Best Local
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SYV_METTH
026861;
[1]
SEQUENCE FROM N.A.
STRAIN=Delta H;
WEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J. Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Bashirzadeh R., Blakely D., Pothier B., Qiu D., Aldredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibbon R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prakhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Pothies G.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S22700; S22700.
InterPro; IPR003005; Amphiphysin.
InterPro; IPR003017; Amphiphysin.
InterPro; IPR006632; BAR.
InterPro; IPR004148; BAR. dom.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curlies requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat valy1-trnA synthetase (EC 6.1.1.9) (Valine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00721; BAR; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01251; AMPHIPHYSIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD003208; Amphiphysin_1;
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03114; BAR; Pfam; PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=187420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPERTIES OF THE
SUBCELLULAR LOCAT
SYNAPTIC VESICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY:
IT IS ALSO FOUND IN
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144
609
682 AA;
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10 84
144 191
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LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Coiled coil.
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Pred. No.
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(Valine--tRNA ligase) (ValRS).
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                                                                                                                                                                                                                                         Dubois J.,
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RESULT 10
PCH7_HUMAN
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HSSP; P96142; IGAX.
InterPro; IPR002300; tRNA-8ynt_1a.
InterPro; IPR001412; tRNA-8ynt_I.
InterPro; IPR002303; tRNA-8ynt_val.
Pfam; PF00133; tRNA-8ynt_1; 1.
Pfam; PF00133; tRNA-8ynt_1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                        PCH7_HUMAN STANDARD; PRT; 1069 AA. 060245; 060246; 060247; Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
-i- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphos)
+ L-valyl-tRNA(Val).
                                                                                                                                      Genomics 49:458-461(1998)
-!- SUBCELLULAR LOCATION: Type I membrane protein
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                       superfamily.";
                                                                                                                                                                                                      BH-protocadherin (PCDH7), a novel member of
                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
MEDLINE=98277460; Pubmed=9615233;
Yoshida K., Yoshicmo-Nakagawa K., Seki N., Sasaki M., Sugano
"Cloning, expression analysis, and chromosomal localization of
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                PCDH7 OR BHPCDH.
                                                                                                                                                                                                                                                                                                                                                                             Protocadherin 7 precursor (Brain-heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0422; valS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
ISOIQ=V0V47--,
Name=C; Synonyms=BH-Pcdh-c;
ISoId=O60245-3; Sequence=VSP_000705, VSP_000706;
ISOId=O60245-3; Expressed predominantly in bra
                                                      Event-Alternative splicing; Named isof
Name-A; Synonyms-BH-Pcdh-a;
IsoId-o60245-1; Sequence=Displayed;
Name-B; Synonyms-BH-Pcdh-b;
IsoId-060245-2; Sequence=VSP_000704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic.
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Similarity 46.7%;
7; Conservation
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Pred. No. 64;
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ATP (BY SIMILARITY)
V; B939720D6D8FF0DB
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                                                                                                                          Named isoforms=3;
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                and heart
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RESULT 11
DNM1_CHICK
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AC Q92072
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DNM1_CHICK
Q92072;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00232; CADHERIN_1; 6.
PROSITE; PS00268; CADHERIN_2; 7.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB006755; BAA25194.1; -.
EMBL; AB006756; BAA25195.1; -.
EMBL; AB006757; BAA25196.1; -.
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GO; 6006887; C:integral to plasma membrane; TAS InterPro; IPR002126; Cadherin.
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PIR; T00042; T00042.
HSSP; P15116; 1NCJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 602988;

    -!- SIMILARITY: Contains 7 cadherin domains.

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nes 9; Conserv
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                                                                                                                                                                    Score 44;
Pred. No.
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SGLEESETPSSKSSSGPRLGALPLPEDNYERTTPDGSVDSR
PLPDVALTGKCTRECDEYGHSDSCWMPVRTSPERKKSQPKL
STFMFVDERGSQEKLANGEAAIMGDRNRNLLNKKLTSSYET
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CADHERIN 6.
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               PRT;
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PIR; JC4172; JC4172.

REBASE; 3020; M.GgaI.

InterPro; IPR00125; BAH.

InterPro; IPR001525; C5_DNA_meth.

InterPro; IPR002857; znf CXXC.

Pfam; PP001426; BAH; 2.

Pfam; PP00145; DNA_methylase; 1.

Pfam; PP0008; zf-CXXC; 1.
ZN FING
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ACT_SITE
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA methyltransferase GgaI) (MCMT) (M.GgaI).

MMT1 OR DNMT OR AIM.

Gallus Gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                            PRINTS; PR00105; C5METTRFRASE.
SMART; SM00439; BAH; 2.
TIGREPAMS; TIGR00675; dcm; 1.
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
Transferase; Methyltransferase; Transcription regulation; Repressor;
DNA-binding; Zinc-finger; Zinc; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities removed a license according to the boundary of the statement of the boundary of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p21WAF1.",
Science 277:1996-2000(1997).
-I-FUNCTION: Methylates CpG residues. Preferentially methylates hemimethylated DNA. It is responsible for maintaining methyla patterns established in development (By similarity). Mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=96172572; PubMed=8586618;

Tajima S., Tsuda H., Wakabayashi N., Asaso A., Mizuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97451025; PubMed=9302295;
Chuang L.S.-H., Ian H.-I., Koh T.-W., Ng H.-H., Xu G., Li B.F.L.;
"Human DNA-(cytosine-5) methyltransferase-PCNA complex as a target for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and expression of a chicken DNA methyltransferase cDNA.";
J. Biochem. 117:1050-1057(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D43920; BAA07867.1; -.
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CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
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                     POLY-GLU.
PHOSPHORYLATION (BY SIMILARITY)
                                                                               BAH 2.
7.5 X 2 AA TANDEM REPEATS OF K-G.
POLY-SER.
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             SIMILARITY.
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SEQUENCE
                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                     Repeat
DOMAIN
                                                                                                      Pfam; PF00514; Armadillo_seg; SMART; SM00185; ARM; 5. PROSITE; PS50176; ARM_REPEAT;
                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by
                                                            DOMAIN
                                                                                           Wnt signaling pathway;
                                                                                                                                         EMBL; D38629; BAA07609.1; -. HSSP; Q02248; 3BCT. InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K., Weisburger J.H., Sugimura T., Nagao M.; "Specific 5'-GGA-3'-->5'-GGA-3'-->6'-GGA-3' mutation of the Apc gene in rat col tumors induced by 2-amino-1-methy1-6-phenylimidazo[4,5-b]pyridine."; Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley, and Fisch MEDLINE=95148647; PubMed=7846077
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning of the rat APC gene and Mamm. Genome 6:746-748(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugimura T., Nagao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Fischer 344/N; TISSUE=Brain; MEDLINE=96116966; PubMed=8563176; Toyota M., Ushijima T., Kakiuchi H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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16-OCT-2001
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                                              DOMAIN
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                                                                                                                                                                                                                                                                                 PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY). SIMILARITY: Contains 7 ARM repeats.
                                                                                                                                                                                                                                                                                                                              FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1 and participates in Wnt signaling. APC activity is correlated wits phosphorylation state (By similarity).
                                                                                                                                                                                                                                                                                                                       SUBUNIT:
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                                                                                          Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                       and Fischer 344/N;
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ARM 2.
ARM 3.
ARM 4.
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Pred. No.
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                                                                                          Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assignment to chromosome 18.";
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                                                                                           Coiled
                                                                                                                                                                                                                                                         a collaboration
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01-AUG-1992
01-AUG-1992
28-FEB-2003
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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MUTAGEN
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REPEAT
DOMAIN
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MEDLINE=92114938; PubMed=1370576;

FOULKES N.S., Melletroem B., Benusiglio E., Sassone-Corsi P.;

"Developmental switch of CREM function during spermatogenesis antagonist to activator.";

Nature 355:80-84(1992).

-1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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"CREM gene: use of alternative DNA-binding d 
antagonists of cAMP-induced transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 64:739-749(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS ALPHA; MEDLINE=91145994; PubMed=1847666;
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                                                                                                                                                    ISOId=P27699-4; Sequence=VSP_000602, VSP_000605, DEVELOPMENTAL STAGE: IN PREMEIOTIC GERM CELLS, EXERAMOUNTS IN THE ANTAGONIST FORM. SUBSEQUENTLY, DURIN SPERMATOGENESIS, THE ISOFORM TAU (ACTIVATOR) IS GEN EXCLUSIVELY AND IN EXTREMELY HIGH AMOUNT.

PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                   PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESPONSE, WHILE ISOFORM TAU IS AN SUBUNIT: BINGE DNA AS A CHMER (BY SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                               Name=Gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Alpha;
IsoId=P27699-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE),
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                                                                                                                                                                                                                                                                                                                                                                             IsoId=P27699-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P27699-1; Sequence=Displayed;
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10; Conserv
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41, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence=VSP_000602, VSP_000603, VSP_000607;
                                                                                                                                                                                                                                                                                                                                                                          Sequence=VSP_000602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulator
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ARM 6.
ARM 7.
SER-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
HIGHLY CHARGED.
C->R: IN AN IQ-INDUCED COLON TUMOR.
C->R: JOHN J CROSS J 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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Pred. No. 2.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA AND GAMMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spermatogenesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                         GENERATED
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                                                                                                                                                                                                                                                                                                                                                                          VSP_000604;
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Best Local S
Matches 8
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InterPro; IPR003102; pKID.
InterPro; IPR004827; TF_bZIP.
Pfam; PF00170; bZIP; 1.
Pfam; PF00173; pKID; 1.
PRINTS; PR00041; LEUZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M60285; AAA17495.1; -.
EMBL; M60285; AAA17496.1; -.
EMBL; M60285; AAA17497.1; -.
PIR; A37944; A37944.
PIR; B37944; B37944.
PIR; C37944; C37944.
PIR; C30827; S20827.
                                                                                       CREM RAT
Q03061;
Q1-JUN-1994
01-JUN-1994
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T01310; --
TRANSFAC; T01314; --
TRANSFAC; T01315; --
TRANSFAC; T01316; --
TRANSFAC; T01602; --
TRANSFAC; T02108; --
TRANSFAC; T02109; --
                                                                                                                                                                                                    LT 14
_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                   CREM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation; Nuclear DNA_BIND 284 305 DOMAIN 311 332 VARSPLIC 39 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC;
Transcription regulation; DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MGI:88495; Crem.
GO:0005667; C:transcription factor complex; IDA
                                                                   responsive
                                                                                                                                                                                                                                                                                           128
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                           DVPGIPKIEEEKSEEEG
                                                                                                                                                                                                                                                                                                                                  EVEDVPKVVEPASEREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 AA;
                                                                                     (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                               STANDARD;
                                                                     element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                36576 MW;
                                                                                                                                                                                                                                                                                                                                                                                            42.6%;
                                                                     modulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Alternative
BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JNA-binding; Activator; Repressor;
                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                  17
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••
                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform Alpha, isoform and isoform Gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKDLYCHKAE (in isoform Alpha)
/FTId=VSP_000607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KECRRRKKEYVKCLESRVAVLEVQNKKLIEELETLKDICSP
KTD -> RECRRKKEYVKCLENRVAVLENQNKTLIEELKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP_000605.
A -> T (in isoform Gamma).
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTId=VSP_000606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VSP 000604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTId=VSP_000603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTId=VSP_000602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DC8F8C8ADD3D219F CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N (in isoform Alpha and isoform
                                                                                                                                                                               341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform Gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                          6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 341;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 15
RF2_CORGL
ID RF2_CORG
AC Q8NS78;

CORGL

STANDARD;

PRT;

368 ₿

B35555

28-FEB-2003 (Rel. 41, 28-FEB-2003 (Rel. 41, 28-FEB-2003 (Rel. 41,

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide chain release factor 2 (RF-2).

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                                                                                                                      Matches
                                                                        Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meyer T.E., Habener J.F.;

"Cyclic AMP response element binding protein CREB and modulator ("Cyclic AMP response element binding protein CREB)

protein CREM are products of distinct genes.";

Nucleic Acids Res. 20:6106-6106(1992).

1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA, BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.

1- SUBCULITIE BINDS BA adimer (By Similarity).

1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                    SEQUENCE
                                                                                                                                  Transcription regulation; DNA-binding; Activator; Repressor; Phosphorylation; Nuclear protein; Alternative splicing. DNA_BIND 284 305 BASIC MOTIF (BY SIMILARITY). DOMAIN 311 332 LEUCINE-ZIPPER (BY SIMILARITY)
                                                                                                                                                                                                                         Pfam; PF00170; bZIP; 1.—
Pfam; PF02173; DKID; 1.
PRINTS; PR00041; LEUZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                           EMBL; Z15158; CAA78857.1; -. PIR; S26686; S26686.
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
MEDLINE=93096608; PubMed=1461747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattua.
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                           PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                                   InterPro; IPR001630;
InterPro; IPR003102;
InterPro; IPR004827;
                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T01919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4;
128
                                                                                                                                                                                                                                                                                                                                                  P03069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q03061-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q03061-4; Sequence=Not described;
M: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q03061-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q03061-1; Sequence=Displayed;
                                                        Similarity
8; Conserv
DVPGIPKIEEEKSEEEG
                            EVEDVPKVVEPASEREG
                                                                                                                    341 AA;
                                                          Conservative
                                                                                                                    36628 MW;
                                                                                                                                                                                                                                                                                Leuzip_CREB.
pKID.
TF_bZIP.
                                                                        42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=Not described;
144
                             17
                                                                                                                    LEUCINE-ZIPPER (BY SIMILA; 1DE752148670125E CRC64;
                                                                        Score 43; DB
Pred. No. 34;
                                                           Mismatches
                                                                                      ۲.
                                                          9
                                                                                      Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
MBL outstation -
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Search completed: August 1, 2003, 18:27:43
Job time: 14 secs
                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                       EMBL; AP005276; BAB98194.1; -.

RAMAR; MF 00094; -; 1.

RINGETPRO; IPR005139; PCRF.

RINGETPRO; IPR000352; Pep_rel_factor_I.

RINGETPRO; IPR000374; PrfB.

R Ffam; PF00462; PCRF; 1.

R Pfam; PF00472; RF-1; 1.

R Pfam; PF00472; RF-1; 1.

R PROSITE; PS00745; RF PROK I; 1.
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRFB OR CGL0801.

Corynebacterium glutamicum (Brevibacterium flavum).

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACTORS FAMILY.
                                                              75 IEDLPIMVELAEEEDG
                                                                              2 VEDVPKVVEPASEREG 17 : | | : | | | | |
                                                                                                                                           42.6%; Score 43; DB 1; Length 368; 50.0%; Pred. No. 37;
                                                                90
                                                                                                                               4; Mismatches
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                    Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                      46.5
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of hits satisfying chosen parameters:
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                   Query
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101
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444
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D84603
E70650
T17946
T24541
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C35147
A55819
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JC5601
JC5602
E81815
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49.317 Million cell updates/sec
                            amphiphysin - chic
valine-tRNA ligase
BH-protocadherin-a
                                              probable transposa amphiphysin - chic
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                      BH; protocadherin P
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ALIGNMENTS

hypothetical protein TP0433 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Apecies: 17eponema pallidum subsp. pallidum (syphilis spirochete)
C;Accession: F71326
C;Accession: F71326
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete
A;Reference number: A71250; MUID:9832770; pMID:9865876
A;Accession: F71326

Gwin) McDo

A;Cross-references: GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65422.1; PID:g332271'A;Experimental source: strain Nichols C;Genetics: R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: G71326
A;Accession: G71326
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-27 <COL> A;Cross-references: GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65421.1; PID:g3322710; A;Experimental source: strain Nichols C;Genetics: hypothetical protein TP0434 - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999 C;Accession: G71326 밁 Ś A;Gene: A; Molecule type: DNA A; Residues: 1-256 < COL> A; Status: preliminary; nucleic acid sequence not shown; translation not shown Matches Query Match Best Local (TP0433 184 EVEDAPKVVEPASEREGGER 203 1 EVEDVPKVVEPASEREGGER Similarity 96.0%; ilarity 95.0%; Conservative 0 Score 97; DB 2; Pred. No. 2.8e-07; 0; Mismatches 1 20 Length 256; Indels 0; Gaps 0 Gwin,

Query Match

81.2%;

Score 82;

DB 2;

Length 227;

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RESULT 5
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A;Residues: 1-153 <MTH>
A;Cross-references: GB:AE000862; GB:AE000666; NID:g2621943; PIDN:AAB85360.1; PID:g262195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fur A;Reference number: A65000; MUID:98037514; PMID:9371463

A;Accession: B69215
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                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84603
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\rho_{\rm t} in the phosphoglucomutase (EC 5.4.2.2) pgmA [similarity] - C?Species: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-184 < STO>
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                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
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                                                                                                                                                                                                                                                                                                             GB:AE002093; NID:g4567228; PIDN:AAD23643.1;
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tive 0; Mismatches
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Pred. No.
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Pred. No. 1
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                    Mycobacterium tuberculosis
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1.
A;Residues: 1-1151 <WIL>
A;Residues: 1-1151 <WIL>
A;Cross-references: EMBL:Z81586; PIDN:CAB04695.1; GSPDB:GN00019; CESP;T05F1.6a
A;Experimental source: clone T05F1
                                                                                      submitted to the EMBL Data Library, A;Reference number: Z19905
A;Accession: T24541
                                                                                                                                                                C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T24541
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T17946
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                                                                                                                                                                                                 hypothetical protein T05F1.6a - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A; Residues: 1-308 <GRA>
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                                                    A; Molecule type: DNA
                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
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submitted to the EMBL Data Library, A.Reference number: Z18806 A.Accession: T17946
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                                                                                                                                                A;Note: A443R
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A443R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: phosphoglucomutase C; Keywords: intramolecular transferase; isomerase; phosphoprotein F; 147/Active site: Ser (phosphoserine intermediate) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:283866; GB:AL123456; NID:g3261691; PIDN:CAB06255.1; PID:g1781145
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                              A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96811.1
A;Experimental source: specific host Chlorella strain NC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein A443R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
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EVEDVPKVVEPASEREGGE 19
                                                  Conservative
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Pred. No. 21;
4; Mismatches
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Pred. No. 16;
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                                                Mismatches
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                                                                                                Length 308;
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November

15-Oct-1999 #text_change 15-Oct-1999

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R; Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; pMID:11130712

A; Accession: D96503
                                                                                                                                                                                                                                              R;Brown, D.P.; Idler, K.B.; Katz, L.
J. Bacteriol. 172, 1877-1888, 1990
A;Title: Characterization of the genetic elements required for site-specific integration A;Reference number: A35147; MUID:90202705; PMID:2180909
A;Accession: C35147
                                                                                                                                                                                                                                                                                                                                                  integrase homolog - Saccharopolyspora erythraea
C;Species: Saccharopolyspora erythraea
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change
C;Accession: C35147
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A; Residues: 1-946 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A;Map position: 1
A;Introns: 9/1; 21/2; 43/3; 186/3; 483/2; 574/3; 611/1; 957/3; 1029/2; 1124/3
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                                                                                                                                                               A;Cross-references: GB:M35138; NID:g152671; PIDN:AAA98345.1; PID:g152674
                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-437 <BRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005173; NID:g8778679; PIDN:AAF79687.1; GSPDB:GN00141
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Best Local
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185
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                                                                                                     Similarity
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EVEDMOLVIKAALERRNGVR 204
                                   EVEDVPKVVEPASEREGGER 20
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Pred. No. 63;
4; Mismatches
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Pred. No.
                                                                                                   Score 46;
Pred. No.
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64;
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Maiti, R.; Marziali
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A;Reference number: S47252
A;Accession: S47253
A;Molecule type: DNA
A;Residues: 1-91,'A',93-99 <CL2>
A;Cross-references: EMBL:Z36897; NID:g534886; PID:g534887
A;Experimental source: clone pCWG106
                                                                                                                                                                              A;Cross-references: GB:AL591985; PIDN:CAC49621.1; PID:g15141108; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T. M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Tille: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: suggested by Southern blot analysis in Ref A55819 C;Keywords: chromosomal protein; DNA binding F;8-13/Region: DNA-binding motif (K/R-G-R-G-R-P) F;75-60/Region: DNA-binding motif (K/R-G-R-G-R-P) F;75-80/Region: DNA-binding motif (K/R-G-R-G-R-P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herroc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95994
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R,Claus, P.; Schulze, E.; Wisniewski, J.R.
submitted to the EMBL Data Library, August 1994
A,Description: Insect proteins homologous to mammalian high mobility group proteins I/Y
                                                                                                                                                    A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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A; Residues: 1-99 < CLA>
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A; Title: Insect proteins homologous to mammalian high mobility
A; Reference number: A55819; MUID:95105193; PMID:7806532
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R;Claus, P.; Schulze, E.; Wisniewsk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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Best Local
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   44.6%;
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   45;
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   Length 178;
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Saddaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PNID:9384377
A;Schroeter, R.; Schroeter, R.; Schroeter, R.; Schroeterium Bacillus subtilis.
                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-798 <FUL>
A;Residues: 1-798 <FUL>
A;Cross-references: EMBL:AF047659; PIDN:AAC04430.1; GSPDB:GN00022; CESP:K07H8.10
A;Experimental source: strain Bristol N2; clone K07H8
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                                                                                                        A; Map position: 4
A; Introns: 205/1; 308/3;
                                                                                                                                                                                                                                                                                                                                                                  R;Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid K07H8.
A;Reference number: Z21264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K07H8.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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  Best Loc
Matches
                                                                                                                                                                 Gene: CESP:K07H8.10
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Best Local Similarity
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Virology 186, 9-14, 1992
Virology 186, 9-14, 1992
A;Title: Channel catfish virus: a new type
A;Title: Channel catfish virus: a new type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ORF72 - ictalurid herpesvirus C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992
C;Accession: G36793
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G36793
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A; Residues: 1-873 <WOE>
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C;Species: Caenorhabditis elegans
C;Date: 20-5e-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
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                                                                                                                                                                C; Superfamily: ictalurid herpesvirus 1 hypothetical protein ORF72
                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1350 <DAV>
A;Cross-references: GB:W75136; NID:g331209; PIDN:AAA88174.1; PID:g331280
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A36804
A; Accession: G36793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to GenBank, January 1992 A; Description: Channel catfish vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Davison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: vacuolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: F35H10.4
A; Introns: 39/3; 709/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid F35H10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Woessner, J.
                                                                                                                                                                                                                                A; Note: neither protein nor nucleic acid sequence is given
                                                                                                                                                                                                                                                      A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                      R;Davison, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U40934; NID:g1072149; PID:g1072154; PIDN:AAA81682.1; CESP:F35H1
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                                                                             44.6%; Score 45; DB 2;
Similarity 50.0%; Pred. No. 1.5e+02
9; Conservative
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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/ Cgm2_6/ptcodata/1/pubpaa/US10C_PUBCOMB.pep:*
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                     15 US-10-036-542-66
15 US-10-036-542-92
15 US-10-036-542-134
15 US-10-036-542-130
10 US-09-864-761-3592
10 US-09-864-761-3592
10 US-09-764-864-1172
11 US-09-752-639-151
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Sequence 134, Appl
Sequence 130, Appl
Sequence 1615, Appl
Sequence 35920, A
Sequence 1172, Appl
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ALIGNMENTS

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44,		44, Ar	e 244	ce 2447,	3889	_	2	Sequence 2, Appli	e 87,	e 50,	e 50,	e 2,	e 2,	e 2,	e 2, 1	Sequence 30, Appl	98,	4.	e 1370	11658	Sequence 35, Appl	_	572	e 34	Sequence 45, Appl	26	е 4,	e ω	Sequence 3, Appli

Sequence 66, Application US/10036542 Phblication No. US20030083481A1 GENERAL INFORMATION: APPLICANT: Birse et al. TITLE OF INVENTION: 25 Human Prostate and Proposition of the Propositi PRIOR APPLICATION NUMBER: 60/194,689 PRIOR FILING DATE: 2000-04-05 Prostate Cancer Associated Proteins

; SEQ ID NO 66 ; LENGTH: 266 ; TYPE: PRT ; ORCANISM: Homo sapiens US-10-036-542-66 Query Match Best Local S Matches 8 238 EIPKVFDPEKERESG 252 4 DVPKVVEPASEREGG 18 Similarity 8; Conser 48.5%; nilarity 53.3%; Conservative 3 Score 49; DB Pred. No. 12; 3; Mismatches 15; Length 266; Indels 0 Gaps

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NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn Ver.

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US-10-036-542-92
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CURRENT APPLICATION NUMBER: US/10/036,542
CURRENT FILING DATE: 2002-01-07
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CURRENT FILING DATE: 2002-01-07
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TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
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PRIOR APPLICATION NUMBER: 60/149,173
PRIOR FILING DATE: 1999-08-17
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PRIOR FILING DATE: 1999-07-21
                                                                                                SOFTWARE: PatentIn
                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/19666
PRIOR FILING DATE: 2000-07-20
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/144,972
PRIOR FILING DATE: 1999-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
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               TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
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                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/149,173
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                                                                                                                                                               APPLICATION NUMBER: 60/194,689
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                                                                                                                                                                                    FILING DATE: 1999-10-06
                                                                                                                                                                                                                                                                      FILING DATE: 1999-08-13
                                                                                                                                                                                                                           FILING DATE: 1999-08-17
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to. US20030083481A1
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53.3%;
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1615
LENGTH: 304
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Best Local Similarity
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SEQ ID NO 130
LENGTH: 288
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Best Local Similarity
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CURRENT FILING DATE: 2002-01-07
CURRENT FILING DATE: PC7/US00/19666
PRIOR APPLICATION NUMBER: PC7/US00/19666
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/144,972
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PRIOR APPLICATION NUMBER: 60/158,004
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PRIOR APPLICATION NUMBER: 60/149,173
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PRIOR APPLICATION NUMBER: 60/148,681
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TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
FILE REFERENCE: PA002P1
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ITTLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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LOCATION: (147)
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53.3%; Pred. No.
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Pred. No.
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13;
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Matches
                                                       SOFTWARE: Annomax
SEQ ID NO 35920
LENGTH: 71
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CURRENT FILING DATE: 2001-05-23
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LOCATION:
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FEATURE:
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: PCT/US01/00661
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Chen, Wensheng
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                                                                                       Sequence Listing
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53.3%; Pred. No.
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APPLICANT:

ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI SAKAKI, YOSHIYUK

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RESULT 8
US-10-156-761-10989
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US-09-764-864-1172
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
Sequence 10989, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1172
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CURRENT FILING DATE: 2001-01-17
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (262
                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (58)
                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 268
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                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                                                                   EEVPEIQEKEEQEEGRER
                                                                                                              EDVPKVVEPASEREGGER
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                                                                                                                                                                                                                               (262)
                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAP TO ACOO6146.2
EXPRESSED IN PLACES
EXPRESSED IN BRAIN
EXPRESSED IN ADULT
EXPRESSED IN FETAL
EXPRESSED IN BT474.
EXPRESSED IN HEART
EXPRESSED IN HEART
EXPRESSED IN HEART
EXPRESSED IN HEART
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EXPRESSED
                                                                                                                                                                                                                                                          Xaa equals
                                                                                                                                                                                                                                                                                                    Xaa equals any
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ED IN ADULT LIVER, SIGNAL = 2.4
SED IN BT474, SIGNAL = 2.1
SED IN HEART, SIGNAL = 1.7
SED IN HEART, SIGNAL = 2.3
SED IN HELAN, SIGNAL = 2.3
SED IN HELAN, SIGNAL = 2.1
SED IN LUNG, SIGNAL = 5.1
SED IN LUNG, SIGNAL = 5.1
SED IN BONE MARROW, SIGNAL = 2.4
SED IN BONE MARROW, SIGNAL = 2.4
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Pred. No. 16;
4; Mismatches
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                                                                                                                                                        Score 44;
Pred. No.
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                                                                                                                                          Mismatches
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RESULT 9
US-09-752-639-151
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Best Local S
Matches 9
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LENGTH: 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15109
                                                   NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Alterin
TITLE OF INVENTION: Factor Receptor
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                           TELEFAX: 65.
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 755 PAGI
CITY: Palo Alto
STATE: CA
                                                                                                                                                            NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/081,385 FILING DATE:
APPLICATION NUMBER: 08/964,747 FILING DATE: 05-NOV-1997 APPLICATION NUMBER: 60/030,761 FILING DATE: 06-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1018
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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                                 ENGTH:
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                amino acid
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                                   1038 amino acids
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05-NOV-1997
single
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47.4%; Pred. No. 1.10
ative 3; Mismatches
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                                                                                                                                                            22000-20577.21
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                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                   TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/984,198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/1079:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
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TELEPAX: 650-494-0792
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FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/0
FILING DATE: 06-NOV-1996
                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                               NAME: Wu, Frank
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER:
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                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                     LENGTH:
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EEVPEIQEKEEQEEGRER
                             EDVPKVVEPASEREGGER 20
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ER: 22000-20577.21
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971
                                                            Score 44; DB 10; Pred. No. 3.2e+02; 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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Pred. No. 3.
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3.2e+02;
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                                                                                                                                      US-09-738-626-6590
                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-764-864-1091
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                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1091
LENGTH.
                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1091, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOPTWARE: PATENTIN VERSION 3.1
SEQ ID NO 109
                                                                                                       Sequence 6590, Application US/09738626 Publication No. US20020197605A1
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Best Local S
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Best Local (
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 109, Application No.
                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/309,395 PRIOR FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. US20030104479Alel Fusion Proteins And Assays For Molecular Bi
FILE REFERENCE: 01-1022-US
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 178
TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Binding domain
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                                                                                                                                                                                                        129 PRLSVPAAPREGGAR 143
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8; Conserv
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8; Conserv
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      ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Premkumar, D. Chen, Yih-Tai
                                                        MIZOGUCHI, HIROSHI
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Pred. No.
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Pred. No.
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RESULT 15
US-09-738-626-4393
; Sequence 4393, Application US/09738626
; Publication No. US20020197605A1
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US-10-102-806-605
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6590
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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SEQ ID NO 6590
LENGTH: 241
                                                                                                   Query Match
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NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                           NAME/KEY: SITE
LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens FEATURE:
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les 9; Conserv
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OZAKI, AKIO
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TATEISHI, NAOKO
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                                                                   Conservative
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56.2%;
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Pred. No.
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                                                                   Mismatches
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GENNERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIXGGUCHI, HIROSHI
APPLICANT: MIXGGUCHI, HIROSHI
APPLICANT: MIXGGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OCAKI, AKIO
TITLE OF INVENTION: NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-012-18
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UF 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UF 99/377484
PRIOR APPLICATION NUMBER: UF 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UF 90/159162
PRIOR APPLICATION NUMBER: UF 90/159162
PRIOR APPLICATION NUMBER: UF 90/280988
INUMBER OF SEQ ID NOS: 7059
INUMBER OF SEQ ID NOS: 70
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /cgn2 6/ptodata/1
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-234-613-45
US-09-233-913-2
US-09-732-210-1401
US-09-732-210-141
US-09-252-991A-2141
US-09-252-991A-2145
US-09-252-991A-2145
US-09-252-991A-2145
US-09-252-991A-32328
US-09-252-991A-32328
US-09-732-210-308
US-09-732-210-308
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US-09-001-951-18
US-08-818-829-18
US-08-363-208-2
US-08-363-208-2
US-08-426-125-8
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US-08-455-355-35-8
US-09-046-894-35
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US-09-252-991A-32898
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US-09-163-748C-7
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29.180 Million cell updates/sec
Sequence 35, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 2, Appl
Sequence 341, Ap
Sequence 3487, Ap
Sequence 21487, Ap
Sequence 21487, Ap
Sequence 11459, A
Sequence 16, Appl
Sequence 308, App
Sequence 183, App
Sequence 183, App
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26148, A
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US-09-134-001C-5584
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	50, Appl	50, Appl	50, Appl	50, Appl	2, Appli	6, Appli	2, Appli	2, Appli	Appli	98, Appl	33084, A	26212, A	22751, A	25831, A	24305, A	29587, A	1402, Ap	T. C. C. C. C.

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5584
                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-163-748C-7
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CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                 APPLICANT: DeBacker, Oliver
APPLICANT: Van den Bynde, Benoit
APPLICANT: Van den Bynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode Member Of The
TITLE OF INVENTION: Pamily, The Proteins Encoded, And Uses Thereof
FILE REFERENCE: LUD 5558
CURRENT APPLICATION NUMBER: US/09/163,748C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 27
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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SEQ ID NO 5584
LENGTH: 801
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TYPE: PRT
ORGANISM: Homo :
FEATURE:
                                                         ENGTH: 117
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Pred. No. 22;
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                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-32898
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US-09-252-991A-26148
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                                                                 Best Loc
Matches
                                                                                                                                                                                  PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32898
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26148
                                                                               Query Match
Best Local S
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Best Local (
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PRIOR APPLICATION NUMBER: US 6
PRIOR APPLICATION NUMBER: 1998-07-27
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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5. 6551795
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                                                                 l Similarity
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VEHVEGVVEFLSRGHG 89
                               VEDVPKVVEPASEREG 17
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WENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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1998-02-18
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                                                               Score 44; DB Pred. No. 18; 0; Mismatches
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Pred. No. 21;
3; Mismatches
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Pred. No. 2.
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US-09-001-951-18
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                                                                                                                                                                                                         Sequence 18, Applicat Patent No. 6268470 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., An
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows95
SOFTWARE: FRSESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,648
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                        APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSIT
TITLE OF INVENTION: DIAGNOSII
TITLE OF INVENTION: GROWTH A
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LENGTH: 747 amino acid
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TITLE OF INVENTION:
                                                                                                      CORRESPONDENCE ADDRESS:
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ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
COUNTRY: US
ZIP: 02110-2804
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Local Similarity 50.0%;
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TELEPAX: 617-542-8906
                                     STATE:
                                                      CITY:
                                                                    STREET:
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ZIP: 02110-2804
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                                                                                    ADDRESSEE:
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225 Franklin
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                                                                                      Richardson,
                                                                                                                                         GROWTH AND
                                                                                                                                                         COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION, AND TREAT!
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Pred. No.
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                                                                                                                                         PROLIFERATION
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COMPUTER READABLE FORM:

CURRENT APPLICATION DATA:

FastSEQ for Windows Version 2.0

COMPUTER: IBM CON OPERATING SYSTEM:

MEDIUM TYPE:

Diskette M Compatible TEM: Windows95

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Query Match
Best Local Similarity
Marches 9; Conserva
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Patent No. 6
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APPLICATION NUMBER: 08/818,829
FILING DATE: 14-MAR-1997
APPLICATION NUMBER: 60/013,438
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/013,438
FILLING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0030
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INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,829
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATH
TITLE OF INVENTION: GROWTH AND PROLIFERATION
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FRAGMENT TYPE:
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internal
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         07334/003001
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Pred. No. 72;
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                                Matches
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Best Local (
                                                              Query Match
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APPLICANT: Murai, No. 9
TITLE OF INVENTION: Art
TITLE OF INVENTION: Rei
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                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                           REGISTRATION NUMBER: 20,152
REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504)275-8689
                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/657,429
PILING DATE: 19-FBB-1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 70815
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Llewellyn A. Proctor, Sr. STREET: 11481 Sheraton Drive
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acid
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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TELEX: 200154
                      42.6%;
Local Similarity 50.0%;
les 6; Conservarion
                                                                                                                                                                                                                                                        NAME: Proctor Sr., Llewellyn A. REGISTRATION NUMBER: 20,152
                                                                                                                                         TYPE: amino acid
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1 EVEDVPKVVEPA 12
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nilarity 50.0%;
Conservative
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Murai, No. 5767366imoto
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Mutant Acetolactate Synthase Gene From
Arabidopsis Thaliana For Conferring Imidazolinone
Resistance To Crop Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18:
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Pred. No. 72;
                                             Score 43; DB
Pred. No. 91;
                                Mismatches
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                                                            Length 670;
                                Indels
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                                                                                                                                                                                                                                                                                                       US-08-426-125-8
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                                                                                                                                                                                                                                                     Sequence 8, Appropriate No. 5853973
                                                                                                                                                                                                                                      Patent No. 5853973
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,429
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: PROCECT ST 110:001177 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                          APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sathasivan, Kanagasabapathi
APPLICANT: Murai, No. 6225105imoto
TITLE OF INVENTION: A Muttant Acetolactate Synthase Gene
TITLE OF INVENTION: Arabidopsis Thaliana For Conferring
TITLE OF INVENTION: Resistance To Crop Plants
                                                                                                                                                                        APPLICANT: Kakefuda, Genichi
APPLICANT: Ott, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 42.6%;
Local Similarity 50.0%;
hes 6; Conservative
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CITY: Baton Rouge,
STATE: LA
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 20,152
REFERENCE/DOCKET NUMBER: 013911-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Proctor Sr., Llewellyn A. REGISTRATION NUMBER: 20,152
                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/137,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                       E: Darby & Darby
805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (504) 275-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 670;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/426,125
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, Joseph
REGISTRATION NUMBER: 3,448
REFERENCE/DOCKET NUMBER: 0646/0A674
REFERENCE/TON INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PACENT PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION WHERE: US/08/455,355
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
ATTORNEY/AGENT INFORMATION:
NAME: RODINBON, JOSEPH
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A674-US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDITOTION NUMBER: 18 / 108/26 125
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kakefuda, Genic
APPLICANT: Ott, Karl-Heinz
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Structure-Based De
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 12.
TELEFAX: 236687
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                                                                                                                                                                                                                                                                                                      STATE:
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5928937
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amino acid
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Stockton, Gera
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Pred. No. 92;
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Query Match
Best Local Similarity
Marches 6; Conserva
                                                                                                                                                                     RESULT 13
US-09-046-894-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILL OF INVENTION: Products
FILE REFERENCE: 3489/1A674-US3
CURRENT APPLICATION NUMBER: US/09/367,512
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 08/426,125
PRIOR FILING DATE: 1995-04-20
PRIOR PPLICATION NUMBER: 08/455,355
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: 06/456/05782
PRIOR APPLICATION NUMBER: 07/US96/05782
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                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
                                                                                                                                                      Sequence 35,
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Patent No. 6576455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: American Cyanamid Company
APPLICANT: Kakefuda, Genichi
APPLICANT: Ott, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu.
APPLICANT: Stockton, Gerald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
                                                                                                    GENERAL INFORMATION: APPLICANT: Ralph,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kwegh, Jae-Gyu.
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide Resistant
TITLE OF INVENTION: Products
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Aral
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Arabidopsis thaliana
              APPLICANT: An, Gang
APPLICANT: O'Hara, Mark S.
APPLICANT: Veltri, Robert
TITLE OF INVENTION: DIAGNO.
TITLE OF INVENTION: PROFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 671
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NUMBER OF SEQUENCES:
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TYPE: amino acid
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227 DVEDIPRIIEEA 238
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                                                                                                                                                      Application US/09046894
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                                                                                               Ralph, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) -753-6237
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                DIAGNOSIS OF DISEASE STATE USING MRNA PROFILES IN PERIPHERAL LEUKOCYTES
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                             Mismatches
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92;
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                                                                      Matches
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Best Local (
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APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:014
                                                                                                                                                                                                                                                         TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 761 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Houston
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727 DTPATSDPLSEEKGGKK 743
                                4 DVPKVVEPASEREGGER 20
                                                         42.6%; Score 43; DB 3; Similarity 41.2%; Pred. No. 1.1e+02; 7; Conservative 4; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Arnold, Wh: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                     Length 761;
                                                                     Indels
                                                                     0
                                                                     Gaps
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RESULT 14 US-08-933-750C-45 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
APPLICATION NUMBER: US/08/933,750C APPLICANT: APPLICANT: APPLICANT: COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett APPLICANT: APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98 CORRESPONDENCE ADDRESS APPLICANT: ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive CITY: Palo Alto STATE: INFORMATION: S Application US/08933750C Au-Young, Janice Yue, Henry Shah, Purvi Hillman, Jennifer L. Bandman, Olga B: Diskette IBM Compatible September 23, 1997 Preeti

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

PF-0356 US

CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:

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CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/933,750
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                          APPLICATION NUMBER:
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6132973
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                                                                                                                                                                                                                                                                                                                                                                                                                                          3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shah, Purvi
                                                                                                                                                                                                                        US/09/234,613
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                                                                                                                        US-09-234-613-45
                                                            Matches
                                                                                        Query Match
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 811 amino acids
                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: LIVRT
CLONE: 2515476
                                                          y Match 42.6%; Score 43; DB 3; Le Local Similarity 41.2%; Pred. No. 1.1e+02; hes 7; Conservative 4; Mismatches 6;
                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lir
777 DTPATSDPLSEEKGGKK 793
                             4 DVPKVVEPASEREGGER 20
                                                                                                                                                                                                                 amino acid
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Gaps

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Search completed: August 1, 2003, 18:38:35 Job time : 30 secs

LENGTH: 811 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVRTUTO4
CLONE: 2515476
US-08-933-750C-45

INFORMATION FOR SEQ ID NO:

45:

TELEFAX: 415-845-4166

SEQUENCE CHARACTERISTICS: LENGTH: 811 amino acid

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Query Match
Best Local Similarity
Matches 7; Conserv

Conservative

4.

Mismatches

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Gaps

0,

42.6%; Score 43; DB 2; 41.2%; Pred. No. 1.1e+02;

Length 811; Indels

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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Gapop 10.0 , Gapext 0.5
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77.428 Million cell updates/sec
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
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and is Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9	80	7	6	ر ت	4	ω	Ŋ	۲	Result No.
77	82	87	96	97	101	101	101	101	Score
76.2	81.2	86.1	95.0	96.0	100.0	100.0	100.0	100.0	% Query Match Length
20	20	20	20	20	432	312	232	20	Length
22	22	22	22	22	22	22	22	22	DB
AAB48321	AAB48330	AAB48320	AAB48328	AAB48329	AAB48316	AAB48318	AAB48317	AAB48327	ID
T. pallidum acidic		T. pallidum acidic	_	•		pallidum		T. pallidum acidic	Description

Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological

WPI; 2001-080711/09.

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AAB80343 AAM41524 AAB57037 AB615624 AAG82199 AB640739 AB6407682 AB6934774 AAG68177 AAG68177 AAG68177 AAG68177 AAG69486 AAG459486 AAG459486 AAG59487 AAG59486	AAB48325 AAB48319 AAB48326 AAG61691 AAG16629 AAG50350 AAM39738 AAB60379 AAB60379 AAB60347
Human prostate can Human prostate can Human prostate can Novel human diagno s. epidermidis ope Staphylococcus epi Novel human diagno Human ORDD protein Arabidopsis thalia Propionibacterium Human liver peptid #265 enco Peptide #261 enco Protein #2621 enco Protein Brain expres Human bone marrow Peptide #2368 enco Peptide #2368 enco Peptide #2368 enco Peptide #2367 enco	llidum aci llidum aci dopsim tha dopsim tha dopsim tha polypepti prostate acid sequ prostate

ALIGNMENTS

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RESULT 1
AAB48327
Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
                                                                               14-JUN-1999;
                                                                                                                 21-DEC-2000.
                                                                                                                                                 Treponema pallidum
                                                                                                                                                                                           T. pallidum acidic repeat protein immunogenic peptide arp 9.
                                                                                                                                                                                                            20-APR-2001 (first entry)
                                                                                                                                                                                                                             AAB48327;
                                                                                                                                                                                                                                            AAB48327 standard; peptide; 20 AA.
                                               Liu H,
                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                14-JUN-2000; 2000WO-US16425
                                                                                                                                 WO200077486-A2
                                              Steiner B,
                                                                                99US-0138981.
                                               Rhodes B;
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      # X & X S S S S S S S S S S S S S X &
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences ABB48319-AAB48330 represent immunogenic peptides of T. pallidum
The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against
                                                                                                                                                         Claim 15;
                                                                                                                                                                                                    Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeprotein of the bacterium and an antibody present in the biological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treponema pallidum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T. pallidum ssp. pertenue (CDC-2) acidic repeat protein (arp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB48317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB48317 standard;
                                                                                                                                                                                                                                                                                                                         Liu H,
                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-2000; 2000WO-US16425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yaws; bejel.
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                                                                                                                                                                                                                                                                                                                                                        US DEPT HEALTH & HUMAN
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                                                                                                                                                     Fig 8; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acidic repeat protein; arp; immunogenic; syphilis;
                                                                                                                                                                                                                                                                                                                         Rhodes B;
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Pred. No. 3.1e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        SERVICES.
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EVEDVPKVVEPASEREGGER 20

Query Match Best Local S Matches 20

Similarity

100.0%; ilarity 100.0%; Conservative

0

Score 101; DB 2 Pred. No. 7e-08; Nismatches

22;

Length 312;

0,

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RESULT 3
AAB48318
ID AAB4
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Best Local
                       The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. The present sequence represents a T. pailidum subspecies endemicum (Bosnia) arp protein.
                                                                                                                                                                                                                                                                Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T. pallidum ssp.endemicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. The present sequence represents a T. pallidum subspecies pertenue (CDC-2) arp protein.
Sequence
                                                                                                                                                                                                                      Claim 15; Fig 10;
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC84649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2000; 2000WO-US16425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yaws; bejel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
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                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVEDVPKVVEPASEREGGER 147
312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0138981.
                                                                                                                                                                                                                     73pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                          Rhodes B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endemicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Bosnia) acidic repeat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 2
Pred. No. 5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                       SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232;
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RESULT 5
AAB48329
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AAB48316
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SAXAXE
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                        The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing sphills, yaws, and bejon diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphills, yaws or bejon caused by TP. The present sequence represents a T. pallidum subspecies pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
            20-APR-2001
                                       AAB48329;
                                                               AAB48329 standard;
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Fig 6; 73pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH)
                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pallidum ssp. pallidum (Ni) acidic repeat protein (arp).
                                                                                                                                  168
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                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                    Similarity
                                                                                                                                                 EVEDVPKVVEPASEREGGER 20
                                                                                                                                                                                                                                                                 protein.
                                                                                                                                  EVEDVPKVVEPASEREGGER 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVEDVPKVVEPASEREGGER 147
                                                                                                                                                                                                                                          432 AA;
                                                                                                                                                                                      Conservative
           (first entry)
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                                                               peptide;
                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pallidum
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                                                                                                                                                                                                 Score 101; DB 2
Pred. No. 1e-07;
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                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                    0;
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                                                                                                                                                                                    Indels
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RESULT 6
AAB48328
X F X B X B X S X X X X B X B X B X A X
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48330 represent immunogenic peptides of T. pallidum
                                                                                                                                Treponema pallidum; acidic repeat protein; arp; immunogenic; syphills; yaws; bejel.
                                                                                                                                                                            T. pallidum acidic
                                                                                                                                                                                                                                                                 AAB48328 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arp protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T. pallidum acidic repeat protein immunogenic peptide arp 11
                                                                       WO200077486-A2
                                                                                                Treponema pallidum
                                                                                                                                                                                                     20-APR-2001 (first entry)
                                                                                                                                                                                                                                       AAB48328;
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                                                                                                                                                                          repeat protein immunogenic peptide arp 10
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                                                                                                                                                                                                                                                                                                                                                                                                                   96.0%;
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Pred. No. 1.4e-08;
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14-JUN-2000; 2000WO-US16425

21-DEC-2000.

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ARESULT 7
AAB48320
ID AAB4
AC AAB4
AC AAB4
AC AAB4
AC T: F
XX Treg
KW Treg
KW Yaws
XX Treg
KW Yaws
XX Treg
XX WO2(
XX II-:
XX III-:
XX III
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pa
yaws; bejel
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                                                                                      Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T. pallidum acidic repeat protein immunogenic peptide arp
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                                                     protein of
                                                                                                                                                                                                                                 Liu H,
                                                                                                                                                                                                                                                                                                                                                  14-JUN-1999;
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                             sample
                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN
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                                                                                                                                                                            2001-080711/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pallidum;
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                                                           the bacterium and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acidic repeat protein; arp; immunogenic; syphilis;
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                                                                                                                                                                                                                                 Rhodes
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Pred. No. 2e-0
1; Mismatches
                                                        an antibody present in
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                                                                                                                                                                                                                                                                                         SERVICES
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                                                        biological
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RESULT 8
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Best Local S
Matches 17
The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing sphills, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphills, yaws or bejel caused by TP. Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP.
                                                                                                                                                                                                                                                                             Detecting Treponema pallidum in blood, saliva, etc., formation of a complex between immunogenic peptides of protein of the bacterium and an antibody present in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T. pallidum acidic repeat protein immunogenic peptide arp 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB48330;
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Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
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                                                                                                                                                                                                                            Claim 15;
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les 17; Conser
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Pred. No.
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5.4e-07;
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Best Local S
Matches 15
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                                                                                                                                     The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with at Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
                                                                                                                                                                                                                                                                                                                                           Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arp
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85.0%;
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Pred. No.
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RESULT 11
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences ABB48319-AAB48330 represent immunogenic peptides of T. pallidum
           Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
                                                         T. pallidum acidic repeat protein immunogenic peptide arp
                                                                                        20-APR-2001
                                                                                                                       AAB48319;
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                                                                                                                                                                                                                                                                                              64.4%; Score 65; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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Treponema pallidum.

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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
 Liu H,
                                                                                                                               WO200077486-A2
                                                                                                                                                     Treponema pallidum.
                                                                                                                                                                               Treponema pallidum; yaws; bejel.
                                                                                                                                                                                                                   T. pallidum acidic repeat protein immunogenic peptide arp
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                                                    14-JUN-1999; 99US-0138981.
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                          (USSH)
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                          US DEPT HEALTH & HUMAN
 Steiner B,
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                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                            acidic repeat protein; arp; immunogenic; syphilis;
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 Rhodes B;
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Pred. No. 0.011;
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RESULT 13
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Matches 11
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05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
25-MAR-1999
01-APR-1999
01-APR-1999
              08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
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                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO:
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